

## SEQUENCE LISTING

<110> FAGAN, RICHARD JOSEPH  
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 RODRIGUES, TANIA MARIA  
 POWER, CHRISTINE  
 DE TIANI, MARIASTELLA

<120> SPLICE VARIANT OF HUMAN PLACENTAL GROWTH HORMONE

<130> C&R-106

<140> US 10/539,962  
 <141> 2005-06-17

<150> PCT/GB03/05594  
 <151> 2003-12-19

<150> GB 0229850.3  
 <151> 2002-12-20

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gtcgcctgta ccagctggca tatgacacct atcaggagtt tgtaagctct tgggtaatgg 180  
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Asp Asn Ala Met Leu Arg Ala Arg Arg Leu Tyr Gln Leu Ala Tyr Asp  
35 40 45

Thr Tyr Gln Glu Phe Val Ser Ser Trp Val Met Glu Ser Ile Pro Thr  
50 55 60

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35              40              45

Leu Ala Tyr Asp Thr Tyr Gln Glu Phe Val Ser Ser Trp Val Met Glu
50              55              60

Ser Ile Pro Thr Pro Ser Asn Arg Val Lys Thr Gln Gln Lys Ser Asn
65              70              75              80

Leu Glu Leu Leu Arg Ile Ser Leu Leu Leu Ile Gln Ser Trp Leu Glu
85              90              95

Pro Val Gln Leu Leu Arg Ser Val Phe Ala Asn Ser Leu Val Tyr Gly
100             105             110

Ala Ser Asp Ser Asn Val Tyr Arg His Leu Lys Asp Leu Glu Glu Gly
115             120             125

Ile Gln Thr Leu Met Trp Arg Leu Glu Asp Gly Ser Pro Arg Thr Gly
130             135             140

Gln Ile Phe Asn Gln Ser Tyr Ser Lys Phe Asp Thr Lys Ser His Asn
145             150             155             160

Asp Asp Ala Leu Leu Lys Asn Tyr Gly Leu Leu Tyr Cys Phe Arg Lys
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 gaaggcatcc aaacgctgat gtggaggctg gaagatggca gcccccgac tgggcagatc 360  
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 Ser Ser Trp Val Met Glu Ser Ile Pro Thr Pro Ser Asn Arg Val Lys  
 35 40 45  
 Thr Gln Gln Lys Ser Asn Leu Glu Leu Leu Arg Ile Ser Leu Leu Leu  
 50 55 60  
 Ile Gln Ser Trp Leu Glu Pro Val Gln Leu Leu Arg Ser Val Phe Ala  
 65 70 75 80  
 Asn Ser Leu Val Tyr Gly Ala Ser Asp Ser Asn Val Tyr Arg His Leu  
 85 90 95  
 Lys Asp Leu Glu Glu Gly Ile Gln Thr Leu Met Trp Arg Leu Glu Asp  
 100 105 110  
 Gly Ser Pro Arg Thr Gly Gln Ile Phe Asn Gln Ser Tyr Ser Lys Phe  
 115 120 125  
 Asp Thr Lys Ser His Asn Asp Asp Ala Leu Leu Lys Asn Tyr Gly Leu  
 130 135 140  
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 145 150 155 160  
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 <223> Primer INSP105-exon2F

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Ser Arg Leu Phe Asp Asn Ala Met Leu Arg Ala Arg Arg Leu Tyr Gln  
 35 40 45  
 Leu Ala Tyr Asp Thr Tyr Gln Glu Phe Glu Glu Ala Tyr Ile Leu Lys  
 50 55 60  
 Glu Gln Lys Tyr Ser Phe Leu Gln Asn Pro Gln Thr Ser Leu Cys Phe  
 65 70 75 80  
 Ser Glu Ser Ile Pro Thr Pro Ser Asn Arg Val Lys Thr Gln Gln Lys  
 85 90 95  
 Ser Asn Leu Glu Leu Leu Arg Ile Ser Leu Leu Leu Ile Gln Ser Trp  
 100 105 110  
 Leu Glu Pro Val Gln Leu Leu Arg Ser Val Phe Ala Asn Ser Leu Val  
 115 120 125  
 Tyr Gly Ala Ser Asp Ser Asn Val Tyr Arg His Leu Lys Asp Leu Glu  
 130 135 140  
 Glu Gly Ile Gln Thr Leu Met Trp Arg Leu Glu Asp Gly Ser Pro Arg  
 145 150 155 160  
 Thr Gly Gln Ile Phe Asn Gln Ser Tyr Ser Lys Phe Asp Thr Lys Ser  
 165 170 175  
 His Asn Asp Asp Ala Leu Leu Lys Asn Tyr Gly Leu Leu Tyr Cys Phe  
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 Arg Ser Val Glu Gly Ser Cys Gly Phe  
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 1 5 10 15  
 tgc ctg tcc tgg ctt caa gag ggc agt gcc ttc cca acc att ccc tta 96  
 Cys Leu Ser Trp Leu Gln Glu Gly Ser Ala Phe Pro Thr Ile Pro Leu

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Ser Arg Leu Phe Asp Asn Ala Met Leu Arg Ala Arg Arg Leu Tyr Gln			
35	40	45	
ctg gca tat gac acc tat cag gag ttt gta agc tct tgg gta atg gag			192
Leu Ala Tyr Asp Thr Tyr Gln Glu Phe Val Ser Ser Trp Val Met Glu			
50	55	60	
tct att cca aca cct tcc aac agg gtg aaa acg cag cag aaa tct aac			240
Ser Ile Pro Thr Pro Ser Asn Arg Val Lys Thr Gln Gln Lys Ser Asn			
65	70	75	80
cta gag ctg ctc cgc atc tcc ctg ctg ctc atc cag tca tgg ctg gag			288
Leu Glu Leu Leu Arg Ile Ser Leu Leu Leu Ile Gln Ser Trp Leu Glu			
85	90	95	
ccc gtg cag ctc ctc agg agc gtc ttc gcc aac agc ctg gtg tat ggc			336
Pro Val Gln Leu Leu Arg Ser Val Phe Ala Asn Ser Leu Val Tyr Gly			
100	105	110	
gcc tcg gac agc aac gtc tat cgc cac ctg aag gac cta gag gaa ggc			384
Ala Ser Asp Ser Asn Val Tyr Arg His Leu Lys Asp Leu Glu Glu Gly			
115	120	125	
atc caa acg ctg atg tgg agg ctg gaa gat ggc agc ccc cgg act ggg			432
Ile Gln Thr Leu Met Trp Arg Leu Glu Asp Gly Ser Pro Arg Thr Gly			
130	135	140	
cag atc ttc aat cag tcc tac agc aag ttt gac aca aaa tcg cac aac			480
Gln Ile Phe Asn Gln Ser Tyr Ser Lys Phe Asp Thr Lys Ser His Asn			
145	150	155	160
gat gac gca ctg ctc aag aac tac ggg ctg ctc tac tgc ttc agg aag			528
Asp Asp Ala Leu Leu Lys Asn Tyr Gly Leu Leu Tyr Cys Phe Arg Lys			
165	170	175	
gac atg gac aag gtc gag aca ttc ctg cgc atc gtg cag tgc cgc tct			576
Asp Met Asp Lys Val Glu Thr Phe Leu Arg Ile Val Gln Cys Arg Ser			
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ccatcgtctg caccagctgg cttttgacac ctaccaggag tttgtaagct cttgggtaat 180
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actgctcaag aactacgggc tgctccactg cttcaggaag gacatggaca aggtcgagac 540
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ctccgcgccc gtcgcctgta ccagctggca tatgacacct atcaggagtt tgtaagctct 180

tgggtaatgg agtctattcc aacaccttcc aacagggtga aaacgcagca gaaatctaac 240

ctagagctgc tccgcatcca aacgctgatg tggaggctgg aagatggcag cccccggact 300

gggcagatct tcaatcagtc ctacagcaag ttgacacaa aatcgacaaa cgatgacgca 360

ctgctcaaga actacgggct gctctactgc ttcaggaagg acatggacaa ggtcgagaca 420

ttcctgcgca tcgtgcagtg ccgctctgtg gagggcagct gtggcttc 468

<210> 35

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<212> DNA

<213> Homo sapiens

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				1				5								
tcc	ctg	ctc	ctg	gct	ttt	ggc	ctg	ctc	tgc	ctg	tcc	tgg	ctt	caa	gag	102
Ser	Leu	Leu	Leu	Ala	Phe	Gly	Leu	Leu	Cys	Leu	Ser	Trp	Leu	Gln	Glu	
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ggc	agt	gcc	ttc	cca	acc	att	ccc	tta	tcc	agg	ctt	ttt	gac	aac	gct	150
Gly	Ser	Ala	Phe	Pro	Thr	Ile	Pro	Leu	Ser	Arg	Leu	Phe	Asp	Asn	Ala	
	25					30					35					
atg	ctc	cgc	gcc	cgt	cgc	ctg	tac	cag	ctg	gca	tat	gac	acc	tat	cag	198
Met	Leu	Arg	Ala	Arg	Arg	Leu	Tyr	Gln	Leu	Ala	Tyr	Asp	Thr	Tyr	Gln	
40					45					50					55	
gag	ttt	gta	agc	tct	tgg	gta	atg	gag	tct	att	cca	aca	cct	tcc	aac	246
Glu	Phe	Val	Ser	Ser	Trp	Val	Met	Glu	Ser	Ile	Pro	Thr	Pro	Ser	Asn	
				60					65					70		
agg	gtg	aaa	acg	cag	cag	aaa	tct	aac	cta	gag	ctg	ctc	cgc	atc	tcc	294
Arg	Val	Lys	Thr	Gln	Gln	Lys	Ser	Asn	Leu	Glu	Leu	Leu	Arg	Ile	Ser	
			75					80					85			
ctg	ctg	ctc	atc	cag	tca	tgg	ctg	gag	ccc	gtg	cag	ctc	ctc	agg	agc	342
Leu	Leu	Leu	Ile	Gln	Ser	Trp	Leu	Glu	Pro	Val	Gln	Leu	Leu	Arg	Ser	
	90						95					100				
gtc	ttc	gcc	aac	agc	ctg	gtg	tat	ggc	gcc	tcg	gac	agc	aac	gtc	tat	390
Val	Phe	Ala	Asn	Ser	Leu	Val	Tyr	Gly	Ala	Ser	Asp	Ser	Asn	Val	Tyr	
	105					110					115					
cgc	cac	ctg	aag	gac	cta	gag	gaa	ggc	atc	caa	acg	ctg	atg	tgg	agg	438
Arg	His	Leu	Lys	Asp	Leu	Glu	Glu	Gly	Ile	Gln	Thr	Leu	Met	Trp	Arg	
120					125				130						135	
ctg	gaa	gat	ggc	agc	ccc	cgg	act	ggg	cag	atc	ttc	aat	cag	tcc	tac	486
Leu	Glu	Asp	Gly	Ser	Pro	Arg	Thr	Gly	Gln	Ile	Phe	Asn	Gln	Ser	Tyr	
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agc	aag	ttt	gac	aca	aaa	tcg	cac	aac	gat	gac	gca	ctg	ctc	aag	aac	534
Ser	Lys	Phe	Asp	Thr	Lys	Ser	His	Asn	Asp	Asp	Ala	Leu	Leu	Lys	Asn	
			155					160					165			
tac	ggg	ctg	ctc	tac	tgc	ttc	agg	aag	gac	atg	gac	aag	gtc	gag	aca	582
Tyr	Gly	Leu	Leu	Tyr	Cys	Phe	Arg	Lys	Asp	Met	Asp	Lys	Val	Glu	Thr	
	170						175					180				
ttc	ctg	cgc	atc	gtg	cag	tgc	cgc	tct	gtg	gag	ggc	agc	tgt	ggc	ttc	630
Phe	Leu	Arg	Ile	Val	Gln	Cys	Arg	Ser	Val	Glu	Gly	Ser	Cys	Gly	Phe	
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